#6 PK

PCT09

RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/830,524   TIME: 17:43:16

Input Set : A:\Neuro431.app
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 3 <110> APPLICANT: Tao, Weng
 4          Wong, Shou
 5          Hickey, William F
 6          Hammang, Joseph P
 7          Baetge, Edward E
 9 <120> TITLE OF INVENTION: Cell Surface Molecule-Induced Macrophage Activation
11 <130> FILE REFERENCE: 19141-543NATL
13 <140> CURRENT APPLICATION NUMBER: 09/830,524
14 <141> CURRENT FILING DATE: 2001-04-26
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/24630
17 <151> PRIOR FILING DATE: 1999-10-21
19 <150> PRIOR APPLICATION NUMBER: 09/178,869
20 <151> PRIOR FILING DATE: 1998-10-26
22 <160> NUMBER OF SEQ ID NOS: 14
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1019
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 gtggagatga aacttgctgt agatgaagaa gaaaatgctg acaataacac aaaggccaat 180
35 gtcacaaaac caaaaaggtg tagtggaagt atctgctatg ggactattgc tgtgatcgtc 240
36 tttttcttga ttggatttat gattggctac ttgggctatt gtaaaggggt agaaccaaaa 300
37 actgagggat ccgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 360
38 cctgaactcc tggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 420
39 atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 480
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41 cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 600
42 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 660
43 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 720
44 cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 780
45 ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 840
46 aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 900
47 gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 960
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52 <211> LENGTH: 331
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <400> SEQUENCE: 2
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60   Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
61               20                    25                    30
63   Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
64           35              -       40                    45
66   Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
67       50                        55                    60
69   Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
70   65           ·                70 ·                  75                    80
72   Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
73                       85                    90                    95
75   Glu Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
76                   100                   105                   110
78   Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
79               115                   120                   125
81   Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
82       130                   135                   140
84   Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
85   145                   150                   155                   160
87   Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
88                   165                   170                   175
90   Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
91               180                   185 ·                 190
93   Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
94           195                   200                   205
96   Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
97 ·     210                   215                   220
99   Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
100  225                   230                   235                   240
102  Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
103                   245                   250                   255
105  Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
106                   260                   265                   270
108  Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
109               275                   280                   · 285
111  Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
112      290                   295                   300
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123  <212> TYPE: DNA
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129  gtggagatga aacttgctgt agatgaagaa gaaaatgctg acaataacac aaaggccaat 180
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131 tttttcttga ttggatttat gattggctac ttgggctatt gtaaaggggt agaaccaaaa 300
132 actgagggat ccgcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 360
133 cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 420
134 agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 480
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136 accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 600
137 gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 660
138 caggtgtaca ccctgccccc atcccgggat gagctgacca gaaccaggt cagcctgacc 720
139 tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 780
140 ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 840
141 tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 900
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149 <213> ORGANISM: Homo sapiens
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153  1               5                  10                  15
155 Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
156              20                  25                  30
158 Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
159          35                  40                  45
161 Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
162       50                  55                  60
164 Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
165  65                  70                  75                  80
167 Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
168                  85                  90                  95
170 Glu Gly Ser Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
171              100                 105                 110
173 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
174              115                 120                 125
176 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
177       130                 135                 140
179 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
180 145                 150                 155                 160
182 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
183              165                 170                 175
185 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
186              180                 185                 190
188 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
189          195                 200                 205
191 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
192          210                 215                 220
194 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
195 225                 230                 235                 240
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197 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
198             245                 250                 255
200 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
201             260                 265                 270
203 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
204         275                 280                 285
206 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
207         290                 295                 300
209 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 305                 310                 315
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232 <223> OTHER INFORMATION: Description of Artificial Sequence:
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235 <400> SEQUENCE: 6
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245 <223> OTHER INFORMATION: Description of Artificial Sequence:
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307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
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313 <400> SEQUENCE: 12
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317 <210> SEQ ID NO: 13
318 <211> LENGTH: 32
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
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332 <212> TYPE: DNA
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336 <223> OTHER INFORMATION: Description of Artificial Sequence:
337        Oligonucleotide primer
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VERIFICATION SUMMARY
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